

2,2,2-Triphenyl-*N*-(2-pyridylmethyl)acetamideLaura R. Whiteaker, Urmila Pal
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Key indicators

Single-crystal X-ray study
 $T = 100$ K
Mean $\sigma(\text{C}-\text{C}) = 0.002$ Å
 R factor = 0.036
 wR factor = 0.092
Data-to-parameter ratio = 14.7For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.The title compound, $\text{C}_{26}\text{H}_{22}\text{N}_2\text{O}$, possesses normal geometric parameters and forms centrosymmetric dimeric associations *via* $\text{N}-\text{H}\cdots\text{N}$ hydrogen bonds.Received 29 June 2006
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Comment

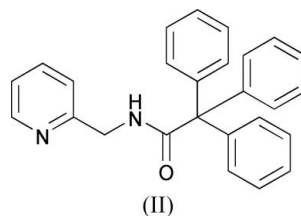
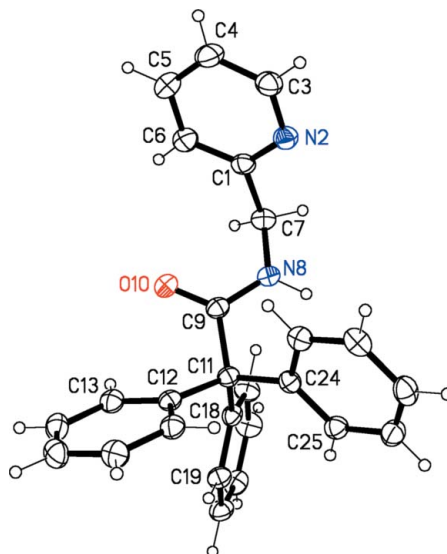
In the preceding paper (Whiteaker *et al.* 2006), we described the crystal structure of the related phenylmethyl-substituted pyridyl amide, $\text{C}_{14}\text{H}_{14}\text{N}_2\text{O}$, (I). Here we present the crystal structure of the triphenylmethyl-substituted title compound (II). Compound (II) (Fig. 1) possesses normal geometric parameters. The hydrogen-bonding scheme in (II) (Table 1) features an $\text{N}-\text{H}\cdots\text{N}$ interaction; inversion symmetry generates a dimeric association of molecules *via* two such bonds (Fig. 2).The hydrogen-bonding scheme in (I) is different and involves $\text{N}-\text{H}\cdots\text{O}$ bonds leading to one-dimensional chains of molecules. This difference may arise for steric reasons; the

Figure 1
View of (II) showing 50% displacement ellipsoids (arbitrary spheres for the H atoms).

bulky triphenylmethyl group in (II) prevents the amide groups from getting close enough to form the hydrogen-bonded chains that occur in (I).

Experimental

Compound (II) was synthesized according to the previously reported procedure (Pal Chaudhuri *et al.*, 2006). X-ray quality crystals of (II) were grown by vapor diffusion of diethyl ether into a dichloromethane solution of (II).

Crystal data

$C_{26}H_{22}N_2O$	$Z = 4$
$M_r = 378.46$	$D_x = 1.271 \text{ Mg m}^{-3}$
Monoclinic, $P2_1/n$	Mo $K\alpha$ radiation
$a = 8.6013 (11) \text{ \AA}$	$\mu = 0.08 \text{ mm}^{-1}$
$b = 17.895 (2) \text{ \AA}$	$T = 100 (2) \text{ K}$
$c = 13.4072 (17) \text{ \AA}$	Block, brown
$\beta = 106.657 (2)^\circ$	$0.58 \times 0.45 \times 0.35 \text{ mm}$
$V = 1977.0 (4) \text{ \AA}^3$	

Data collection

Bruker APEX CCD diffractometer	20831 measured reflections
ω scans	3897 independent reflections
Absorption correction: multi-scan	3660 reflections with $I > 2\sigma(I)$
SADABS (Sheldrick, 2002)	$R_{\text{int}} = 0.025$
$T_{\text{min}} = 0.956$, $T_{\text{max}} = 0.973$	$\theta_{\text{max}} = 26.0^\circ$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.046P)^2 + 0.7P]$
$R[F^2 > 2\sigma(F^2)] = 0.036$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.092$	$(\Delta/\sigma)_{\text{max}} = 0.001$
$S = 1.01$	$\Delta\rho_{\text{max}} = 0.25 \text{ e \AA}^{-3}$
3897 reflections	$\Delta\rho_{\text{min}} = -0.21 \text{ e \AA}^{-3}$
266 parameters	Extinction correction: <i>SHELXL97</i>
H atoms treated by a mixture of independent and constrained refinement	Extinction coefficient: 0.0262 (18)

Table 1

Hydrogen-bond geometry (\AA , $^\circ$).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N8-H8\cdots N2^i$	0.903 (14)	2.081 (14)	2.9544 (14)	162.4 (12)

Symmetry code: (i) $-x + 1, -y + 1, -z + 1$.

The C-bound H atoms were placed in idealized locations ($C-H = 0.95-0.99 \text{ \AA}$) and refined as riding, with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{C})$ or $1.5U_{\text{eq}}(\text{methyl C})$. The N-bound H atom was located in a difference map and its position was refined freely with $U_{\text{iso}}(\text{H}) = 1.2U_{\text{eq}}(\text{N})$.

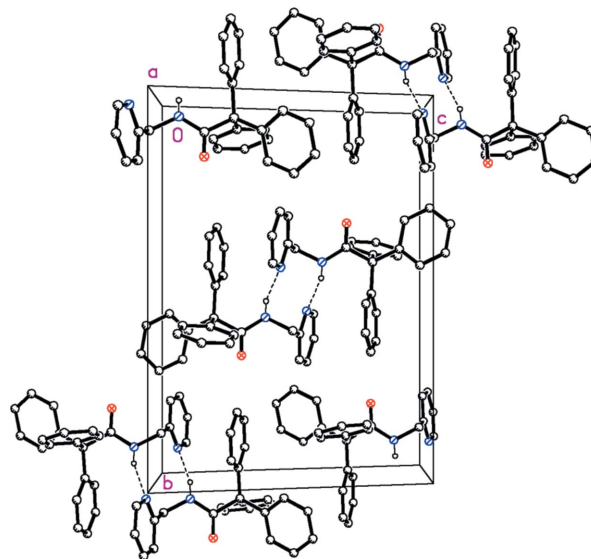


Figure 2

The molecular packing of (II), viewed along the a axis. H atoms have been omitted for clarity, except for those involved in hydrogen bonds (dashed lines).

Data collection: *SMART* (Bruker, 1998); cell refinement: *SAINT* (Bruker, 1998); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 2000); software used to prepare material for publication: *SHELXTL*.

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